

Figure 1

1 GGAAGTCAGCAGGCCGTTGGGAGGGGTGGCGGGAAATTAGCGGGCGGCAGC
51 AGCCCCAGCCCTCAGAGAGACAGCAGAAAGGGAGGGAGGGTGGCTGG
101 GGGGACAGCCCCACCATTCC'TACCGCTATGGGCCAACCTCCACTCC
151 CACCTCCCCTCCATCGGCCGGCTAGGACACCCCCAAATCCCGTCCGCC
201 CCTTGGCACCGACACCCCCGACAGAGACAGACACAGCCATCCGCCACCA
251 CCGCTGCCAGCCCTGGCTGGGCCAGGGCCAGCCCCAGGCCCTAC
301 CCCTCTGAGGTGGCCAGA ATG GAT TTG TGG CCA GGG GCA TGG
Met Asp Leu Trp Pro Gly Ala Trp
343 ATG CTG CTG CTG CTC TTC CTG CTG CTC CTC C
Met Leu Leu Leu Leu Phe Leu Leu Leu Phe L
10
20
380 TG CTG CCC ACC CTG TGG TTC AGC CCC AGT GCC AAG
eu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala Lys
30

Figure 1 (continued)

418 TAC TTC TTC AAG ATG GCC TTC TAC AAT GGC TGG ATC C
Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile L
40

455 TC TTC CTG GCT GTG CTC GCC ATC CCT GTG TGT GCC GTG
eu Phe Leu Ala Val Leu Ala Ile Pro Val Cys Ala Val
50

493 CGA GGA CGC AAC GTC GAG AAC ATG AAG ATC TTG CGT C
Arg Gly Arg Asn Val Glu Asn Met Lys Ile Leu Arg L
60

530 TA ATG CTG CTC CAC ATC AAA TAC CTG TAC GGG ATC CGA
eu Met Leu Leu His Ile Lys Tyr Leu Tyr Gly Ile Arg
80

Figure 1 (continued)

568 GTG GAG GTG CGA GGG GCT CAC CAC TTC CCT CCC TCG C
Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser G
90
605 AG CCC TAT GTT GTT GTC TCC AAC CAC CAG AGC TCT CTC
Iln Pro Tyr Val Val Ser Asn His Gln Ser Ser Leu
100
643 GAT CTG CTT GGG ATG ATG GAG GTA CTG CCA GGC CGC T
Asp Leu Leu Gly Met Met Glu Val Leu Pro Gly Arg C
110
680 GT GTG CCC ATT GCC AAG CGC GAG CTA CTG TGG GCT GGC
ys Val Pro Ile Ala Lys Arg Glu Leu Leu Trp Ala Gly
120
130

Figure 1 (continued)

718 TCT GCC GGG CTG GCC TGC TGG CTG GCA GGA GTC ATC T
Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val Ile P
140

755 TC ATC GAC CGG AAG CGC ACG GGG GAT GCC ATC AGT GTC
he Ile Asp Arg LYS Arg Thr GLY Asp Ala Ile Ser Val
150

793 ATG TCT GAG GTC GCC CAG ACC CTG CTC ACC CAG GAC G
Met Ser Glu Val Ala Gln Thr Leu Leu Thr Gln Asp V
160

830 TG AGG GTC TGG GTG TTT CCT GAG GGA ACG AGA AAC CAC
al Arg Val Trp Val Phe Pro Glu Gly Thr Arg Asn His
180

Figure 1 (continued)

868 AAT GGC TCC ATG CTG CCC TTC AAA CGT GGC GCC TTC C
Asn Gly Ser Met Leu Pro Phe Lys Arg Gly Ala Phe H
190

905 AT CTT GCA GTG CAG GCC CAG GTT CCC ATT GTC CCC ATA
is Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
200

943 GTC ATG TCC TCC TAC CAA GAC TTC TAC TGC AAG AAG G
Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys G
210

980 AG CGT CGC TTC ACC TCG GGA CAA TGT CAG GTG CGG GTG
lu Arg Arg Phe Thr Ser Gly Gln Cys Gln Val Arg Val
220

230

Figure 1 (continued)

1018	CTG CCC CCA GTG CCC ACG GAA GGG CTG ACA CCA GAT G	
	Leu Pro Pro Val Pro Thr Glu Gly Leu Thr Pro Asp A	
	240	
1055	AC GTC CCA GCT CTG GCT GAC AGA GTC CGG CAC TCC ATG	
	Ser Val Pro Ala Leu Ala Asp Arg Val Arg His Ser Met	
	250	
1093	CTC ACT GTT RTC CGG GAA ATC TCC ACT GAT GGC CGG G	
	Leu Thr Val Phe Arg Glu Ile Ser Thr Asp GLY Arg G	
	260	
1130	GT GGT GGT GAC TAT CTG AAG CCT GGG GGC GGT GGG	
	Lys GLY GLY Asp Tyr Leu Lys Pro GLY GLY GLY 280	
1168	TGA ACCCTGGCTCTGAGCTCCCTCATCTGTCCCCATCTGCCTCCC	
1216	CACACTACCCACCCAGTGGCCCTGAAGCAGGGCCAACCCCTTCCCT	
1266	GTCTCCCTCTCCCCACTTATTCTCCCTTGGAATCTCAACTTCTGAA	

Figure 1 (continued)

1316 GTGAATGTGGATAACAGGCCACTCCTGCCATTTGCCCCCATCCATTGG
1366 ACTCTTGCCTCGGTGCAGTTCCACTCTTGACCCCCACCTCCTACTGTCT
1416 TGTCTGTGGACAGTTGCCTCCCTCATCCTCCAGTCAGCCTACAC
1466 AAGGGAGGGAAACATCCATCCCCCAGTGGAGTCTCCATGTTGGTCTT
1516 CTCTACCCCCCTAACCCCCCACATTGGCCAGTGGACTCATCCATTCTTTGGAA
1566 ACAAAATCCCCCACTCCAAGTCCATGGATTCAAATGGACTCATCCATT
1616 TGTGAGGAGGACTTCTGCCCTCTGGCTGGAAAGCTGATAACCTGAAGCACT
1666 CCCAGGGCTCATCCCTGGAGCTTTCCCTCAGCACCTTCACCTTCCCAG
1716 TGTAGCCTCCTGTCACTGGGGCTGGACCCCTTAATTAGAGGTCTCAT
1766 GCCTGCCCTTGCCTCAGATGCCAGGGTCACTCTGGATAACCAGT
1816 TCAGTCTCCACATTCTGGTTTCTGTCCCCATAGTACAGTTCTCAGTGT
1866 GACATGACCCACCCAGCCCCCTGCAGCCCTGCTGACCATCTCACAGAC
1916 ACAAGGGAGAAGCAGACATCAGGTGCTGCACTTCTGCCCTGG
1966 GGAGTTGGGGAAAGGAACGAACCCCTGGCTGGAGGGATAGGAGGGCTTTT

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Figure 1 (continued)

2016 AATTATTCTTTCTGTGAGGCTTCCCCCTCTGAGCCAGTTCA
2066 TTTCTTCCTGGTGCATTAGCCACTCCCTGCTCACTCCAGACCTGTT
2116 CCCACAACTGGGAGGTAGGCTGGAGCAAAGGAGGGTGACCCAG
2166 TTTTGCCTGGTTGGTTATTATAATTATCTGGATAACAGCAAAAAACTG
2216 AAAATAAAGAGAGAGAAAAAAA

Figure 2

Human LPAAT	1	<u>MDLWPGAWM-</u>	10	<u>LLLILF</u>	20	<u>LL-LLFLLPT</u>	30	<u>WFCSPSAKY</u>	40	<u>F-----FKMA</u>
Yeast LPAAT	1	<u>MSV-IGRFLY</u>		<u>YLRSVL-VVL</u>		<u>AL-AG-----</u>		<u>C-----</u>		<u>G-----</u>
E. coli LPAAT	1	<u>M-----</u>		<u>M-----</u>		<u>LYIF</u>		<u>RL-TITVIYS</u>		<u>-----</u>
Maize LPAAT	1	<u>MAI-----</u>		<u>PLVILVVL</u>		<u>PLGLLFLISG</u>		<u>LIVNAIQAVL</u>		<u>FVTIRPFSKS</u>
			60		70		80		90	
Human LPAAT	51	<u>FYNGWILFLA</u>		<u>VIAIIPVCavr</u>		<u>GRNVENMKIL</u>		<u>RIMLHLIKYL</u>		<u>-YGIIRVEVRG</u>
Yeast LPAAT	51	<u>FY-----G</u>		<u>VIASTLCTLI</u>		<u>GKQHILAQWIT</u>		<u>ARCFYHVMKL</u>		<u>MLGLDV-----K</u>
E. coli LPAAT	51					<u>PRNPKHVATF</u>		<u>GHMFGRLAPL</u>		<u>-FGLKVECRK</u>
Maize LPAAT	51	<u>FYRRINRFLA</u>		<u>EL-----</u>				<u>WLQLWVWWDW</u>		<u>WAGVKVQLHA</u>
			110		120		130		140	
Human LPAAT	101	AHHF-PPSQ-		<u>PYVVVSNHQ</u>		<u>SSLDLILGMME</u>		<u>VL-----PGRC</u>		<u>-VPI-AKREL</u>
Yeast LPAAT	101	VVGE-ENLAK		<u>KPYIMJANHQ</u>		<u>STLDIFMLGR</u>		<u>IF-----PPGCT</u>		<u>-----VTAKKSL</u>
E. coli LPAAT	101	PTDA-ESYG-		<u>-NAYTIANHQ</u>		<u>NNYDMVTASN</u>		<u>IVQ-PP-----</u>		<u>TVTV-GKKSL</u>
Maize LPAAT	101	DEETYRSMGK		<u>EHALLISNHR</u>		<u>SDIDWL-IGW</u>		<u>ILAQRSGCLG</u>		<u>STLAVMVKKS</u>
			160		170		180		190	
Human LPAAT	151	<u>LWAGSAGLAC</u>		<u>W---LAGVIF</u>		<u>IDRKRTGDAI</u>		<u>SVMSEVAQTL</u>		<u>LTQDVRVWV-</u>
Yeast LPAAT	151	<u>KYVPPFLG</u>		<u>WEMALSGTYE</u>		<u>LDRSKROEAJ</u>		<u>DTLNKGLENV</u>		<u>KKNKRALWV-</u>
E. coli LPAAT	151	<u>LWIPFFGQLY</u>		<u>W---LTGNLL</u>		<u>IDRNNNRTKAH</u>		<u>GTIAEVVNHF</u>		<u>KKRRISIWM-</u>
Maize LPAAT	151	<u>KFLPVIGSM</u>		<u>WF---AEYLF</u>		<u>LERS-WAKDE</u>		<u>KTLKWGLQRL</u>		<u>KDFPRPFWLA</u>
			210		220		230		240	
Human LPAAT	201	<u>-FPEGTRNHN</u>		<u>GS-----</u>						<u>250</u>
Yeast LPAAT	201	<u>-FPEGTRSYT</u>		<u>SEL-----</u>				<u>T</u>		<u>MLPFFKKGAFH LAQQGKIPIV</u>
E. coli LPAAT	201	<u>-FPEGTRSRG</u>		<u>RGL-----</u>						<u>-LPFKTGAFH AAIAAGVPII</u>
Maize LPAAT	201	<u>LFVEGTRFTP</u>		<u>AKLIAAQEYA</u>		<u>ASQGLPAPRN</u>		<u>VLIPRTKGKV</u>		<u>SAVSIMRDFV</u>

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Figure 2 (continued)

Human LPAAT	251	<u>PIVMSSYQDF</u>	<u>YCKKERRFTS</u>	<u>GQCQVRVLPP</u>	<u>VPTEGLTPDD</u>	<u>VPALADR</u>	300
Yeast LPAAT	251	<u>PVVVSNTSTL</u>	<u>VSPKIGVFNRL</u>	<u>GCMIVRILKP</u>	<u>ISENLTIKDK</u>	<u>IGEFAEK</u>	
E. coli LPAAT	251	<u>PVCVSTTSNK</u>	<u>I--NLNRLHN</u>	<u>GLVIVEMLPP</u>	<u>IDVSQYQGKDQ</u>	<u>VRELAAH</u>	
Maize LPAAT	251	<u>PAYDTT--V</u>	<u>IVPKDSPQPT</u>	<u>MRLILKGQSS</u>	<u>VIHVRMKRHA</u>	<u>MSEMPKSDED</u>	
	260	270	280	290	300		
Human LPAAT	301	---	310	320	330	340	350
Yeast LPAAT	301	---	VRHSMLT	V-F	REI	GDYLKKP	GGG
E. coli LPAAT	301	---	VRDQMVD	T-L	KEI	GYSPAN	G*
Maize LPAAT	301	---	CRSIMEQK-I	AELDKEVAE-	--REAA	GK	V*
	301	VSKWCKDIFV	AKDALLDKHL	ATGTFDEEIR	PIGRPVKSLL	VTLFWSCLLL	
	360	370	380	390	400		
Human LPAAT	351	...	351	351	351	351	351
Yeast LPAAT	351	-- <u>ATEY</u> --A	<u>AL</u>	--Q	HDKKVNKKIK	NEPVPSVSIS	NDVNNTNHNEGS
E. coli LPAAT	351	...	351	351	351	351	351
Maize LPAAT	351	<u>FGAIEFFKWT</u>	<u>QLLSTWRGVA</u>	<u>FTAAGMALVT</u>	<u>GVMHVFIMFS</u>	<u>QA-----ERS</u>	
	410	420	430	440	450		
Human LPAAT	401	...	401	401	401	401	401
Yeast LPAAT	401	<u>S</u>	401	<u>S</u>	<u>KKMH</u>	*	
E. coli LPAAT	401	...	401	401	401	401	401
Maize LPAAT	401	SSARAARNRV	KKE*	SSARAARNRV	KKE*	SSARAARNRV	KKE*

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Figure 3

10 20 30 40 50 60
GGAGGGAGCT GGCGGCCG TCGGGGCCG GGCGGGCCA TGGAGCTGTG GCCGTGTCTG

70 80 90 100 110 120
GCCGGGGCC TGCTGTTGCT GCTGCTGCTG GTGCAGCTGA GCCGGGGCC CGAGTTCATAC

130 140 150 160 170 180
GCCAAGGTTCG CCCTTGTAATG CGCGCTGTGC TTCAACGGTGT CCGCCGTGGC CTGGCTCGTC

190 200 210 220 230 240
TGCCCTGCTGT GCCACGGCGG CCGGACGGTG GAGAACATGA GCATCATCGG CTGGTTCGTG

250 260 270 280 290 300
CGAAGCTTCA AGTACTTTTA CGGGCTCCGC TTCAAGGGTGC GGGACCCGGC CAGGCTGCAG

310 320 330 340 350 360
GAGGCCCGTC CCTGTGTCAAT CGTCTCCAAC CACCAAGAGCA TCCTGGACAT GATGGGCCTC

370 380 390 400 410 420
ATGGAGGTCC TTCCGGAGCG CTGGCTGCAG ATCGCCAAGC GGGAGCTGCT CTTCCCTGGGG

430 440 450 460 470 480
CCCGTGGGCC TCATCATGTA CCTCGGGGGC GTCTTCTTCA TCAACGGCA GCGCTCTAGC

490 500 510 520 530 540
ACTGCCATGA CAGTGATGGC CGACCTGGC GAGGCCATGG TCAGGGAGAA CCTCAAAGTG

Figure 3 (continued)

550	560	570	580	590	600
TGGATCTATC	CCGAGGGTAC	TCGCAACGAC	AATGGGGACC	TGCTGCCTTT	TAAGAAGGGC
610	620	630	640	650	660
GCCTTCTTAC	TGGCA GTCCA	GGCACAGGTG	CCCATCGTCC	CCGTGGTGTAA	CTCTTCCCTTC
670	680	690	700	710	720
TCCTCCTTCT	ACAAACACCAA	GAAGAACGTTT	TTCACTTCAG	GAACAGTCAC	AGTGCAGGTG
730	740	750	760	770	780
CTGGAAAGCCA	TCCCCCACCAG	CGGGCTCACT	GGGGGGACG	TCCCTGGGCT	CGTGGACACC
790	800	810	820	830	840
TGCCACCGGG	CCATGAGGAC	CACCTTCCTC	CACATCTCCA	AGACCCCCCA	GGAGAACGGG
850	860	870	880	890	900
GCCACTGCGG	GGTCTGGCGT	GCAGCCGGCC	CAGTAGCCCCA	GACCACGGCA	GGGCATGACC
910	920	930	940	950	960
TGGGGAGGGC	AGGGTGAAGC	CGATGGCTGG	AGGATGGCA	GAGGGAACTC	CTCCCGGCTT
970	980	990	1000	1010	1020
CCAAATACCA	CTCTGTCCGG	CTCCCCCAGC	TCTCACTCAG	CCCGGGAAAGC	AGGAAGCCCC
1030	1040	1050	1060	1070	1080
TTCTGTCACT	GGTCTCAGAC	ACAGGGCCCT	GGTGTCCCC	GCAGGGGGCT	CAGCTGGACC

Figure 3 (continued)

1090	1100	1110	1120	1130	1140
CTCCCCGGC	TCGAGGGCAG	GGACTCGGCC	CCACGGCACC	TCTGGGNGC	GGGNTGATAA
1150	1160	1170	1180	1190	1200
AGATGAGGCT	TGCGGCTGTG	GCCCGCTGGT	GGGCTGAGCC	ACAAGGGCCC	CGATGGCCCA
1210	1220	1230	1240	1250	1260
GGAGCAGATG	GGAGGACCCC	GAGGCCAGGA	GTCCCAGACT	CACGCACCCCT	GGGCCACAGG
1270	1280	1290	1300	1310	1320
GAGCCGGAA	TCGGGGCCTG	CTGCTCCTGC	TGGCCTGAAG	AATCTGTGG	GTCAAGCACTG
1330	1340	1350	1360	1370	1380
TACTCCGTTG	CTGTTTTTT	ATAAACACAC	TCTTGAAAA	AAAAAAA	AAAAAAA
1390	1400	1410	1420	1430	1440
AAA.....

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Figure 4

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Figure 4 (continued)

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Figure 4 (continued)

510	520	530	540	
CTG GGC GAG CGC ATG GTC AGG GAG AAC CTC AAA GTG TGG ATC TAT				
Leu Gly Glu Arg Met Val Arg Glu Asn Leu Lys Val Thr Ile Tyr				
160	170			
550	560	570	580	590
CCC GAG GGT ACT CGC AAC GAC AAT GGG GAC CTG CCT CCT TTT AAG				
Pro Glu Gly Thr Arg Asn Asp Asn Gly Asp Leu Leu Pro Phe Lys				
	180			
600	610	620	630	
AAG GGC GCC TTC TAC CTG GCA GTC CAG GCA CAG GTG CCC ATC GTC				
Lys Gly Ala Phe Tyr Leu Ala Val Gln Ala Gln Val Pro Ile Val				
190			200	
640	650	660	670	680
CCC GTG GTG TAC TCT TCC TTC TCC TCC AAC ACC AAG AAG				
Pro Val Val Tyr Ser Ser Phe Ser Ser Phe Tyr Asn Thr Lys Lys				
210				
690	700	710	720	
AAG TTC TTC ACT TCA GGA ACA GTC ACA GTG CAG GTG CTG GAA GCC				
Lys Phe Phe Thr Ser Gly Thr Val Val Gln Val Leu Glu Ala				
220	230			

Figure 4 (continued)

730	740	750	760	770
ATC CCC ACC AGC GGC CTC ACT GCG GCG GAC CCT GCG CTC GTG				
Ile Pro Thr Ser Gly Leu Thr Ala Ala Asp Val Pro Ala Leu Val				
			240	
780	790	800	810	820
GAC ACC TGC CAC CGG GCC ATG AGG ACC ACC TTC CTC CAC ATC TCC				
Asp Thr Cys His Arg Ala Met Arg Thr Thr Phe Leu His Ile Ser				
	250		260	
820	830	840	850	860
AAG ACC CCC CAG GAG AAC GGG GCC ACT GCG GGG TCT GGC GTG CAG				
Lys Thr Pro Gln Glu Asn Gly Ala Thr Ala Gly Ser Gly Val Gln				
		270		
870	880	890	900	910
CGG GGC CAG TAG CCCAGACCACGCCAGGGCATGACCTGGGGAGGGCAGGTGGAAGC				
Pro Ala Gln ***				
		920		
940	950	960	970	980
CGATGGCTGGGGATGGGCAGAGGGACTCCTCCGGCTTCCAATACCACTGTCCGG				
990	1000	1010	1020	1030
CTCCCCCAGCTCTCACTCAGCCCCGGAAAGCAGGGCCCTTCTGTCACTGGTCTCAGAC				
1050	1060	1070	1080	1090
ACAGGGCCCTGGTGTCCCCTGCAAGGGGCTCAGCTGGACCCCTCCGGCTCGAGGGCAG				

Figure 4 (continued)

1110	1120	1130	1140	1150	1160
	GGACTCGGCCACGGCACCTCTGGGNCTGGGNTGATAAAGATGAGGCTTGCGGCTGTG				
1170	1180	1190	1200	1210	1220
	GCCCGCTGGTGGCTGAGCCACAAGGCCCGATGGCCAGATGGGAGGACCCC				
1230	1240	1250	1260	1270	1280
	GAGGCCAGGAGTCCCAGACTCACGGCACCCCTGGGCCACAGGGAGCCGGAAATCGGGCCTG				
1290	1300	1310	1320	1330	1340
	CTGCTCCTGCTGGCCTGAAGAATCTGTGGGGTCAGGCACCTGTACTCCGTGCTTTTTT				
1350	1360	1370	1380		
	ATAAACACACTCTGGAAAAAAA	AAAAAAA			

Figure 5

Alignment of LPAAT Sequences.

	10	20	30	40	50	
Human LPAAT- β	1	-----	-----	-----	-----	MEL WPC----LA AAILLLVV
Human LPAAT- α	1	-----	-----	-----	-----	MDL WPGAWMLLL IFLILLFLLP
Yeast LPAAT	1	-----	-----	-----	-----	MSV --IGRFLYYL RSVIWWLALA
E. coli LPAAT	1	-----	-----	-----	-----	-----
H. influenzae	1	-----	-----	-----	-----	-----
S. typhimurium	1	-----	-----	-----	-----	-----
L. douglassi	1	MAKIRTSS-L RNR-----	-----	-----	-----	RQIKP AVAATAD-D DKDGFMV--
C. nucifera	1	MDASGASSFTL RGRCLESCFK ASFQMSQPKD AAGQPSRRPA DADDFTVDD	-----	-----	-----	-----
	60	70	80	90	100	
Human LPAAT- β	51	QL---SRAAE FYAKVAL-YC ALGFTVSAVA SLVCLLCHGG RTVENM-SII	-----	-----	-----	-----
Human LPAAT- α	51	TIWFCSEAK YFFKMAF-YN GWIIFLAVIA TPVCAV--RG RNVENM-KIL	-----	-----	-----	-----
Yeast LPAAT	51	G---CG--- FY-----	-----	-----	-----	GYIA SLLCTLIGKQ HLAQWT-TAR
E. coli LPAAT	51	MLYI FRILIVTVIYS ILVC--VFG SYCYCLFS PRN PKHV---ATF	-----	-----	-----	-----
H. influenzae	51	MLKL LRIFMVLICC ILIC---VLG TLYSFIREKN PSNV---GIV	-----	-----	-----	-----
S. typhimurium	51	MLYI FRILIVTVIYS ILVC--VFG SYCYCLFS PRN PKHV---ATF	-----	-----	-----	-----
L. douglassi	51	LLSC EKTFYCEAFT VLIITAVAWG LTIVLILLWPW VMTRIGNY	-----	-----	-----	-----
C. nucifera	51	DRWITIVLISV VRRAACEFL-- SMMVTTIIVWN MIMIILLPPWP YARIROQNY	-----	-----	-----	-----

Figure 5 (continued)

Human LPAAT- β	101 <u>GWFVRSFKY</u> - --F <u>YGLRFEV</u> RDPRRLQEAR <u>PCVTVSNHQ</u> I <u>LDMGILMEV</u>	110	120	130	140	150
Human LPAAT- α	101 <u>RLMTLHHKY</u> - --L <u>YGTRVEV</u> RGAHHPPSQ <u>PYVVVSNHQ</u> S <u>DILLGMMEV</u>	101				
Yeast LPAAT	101 CFY-H <u>MMKL</u> - --M <u>LGLDYKV</u> V <u>GEENLAK-K</u> P <u>YIMIANHQ</u> T <u>LDDIFMLGR</u> I	101				
E. coli LPAAT	101 <u>GHMFGR</u> L--- <u>APLFGLKVEC</u> R <u>KPTDAE</u> S <u>Y</u> G N <u>AYTIANHQ</u> N <u>NYDMVTA</u> S <u>M</u>	101				
H. influenzae	101 <u>ARWFGR</u> L-FT <u>YPLFGLKVEH</u> R <u>IPQQDQKQIS</u> R <u>AUYTIGNHQ</u> N <u>NYDMV</u> TIS <u>M</u>	101				
S. typhimurium	101 <u>GHMFGR</u> L-FT <u>APLFGLKVEC</u> R <u>KPADAEN</u> Y <u>G</u> N <u>AYTIANHQ</u> N <u>NYDMV</u> TAA <u>N</u>	101				
L. douglassii	101 <u>GHVTCRM</u> L-FT <u>ITWYGIPIKI</u> Q <u>GSEHKR</u> K <u>R</u> A I <u>FTYTSNHAS</u> P <u>IDAFFV</u> M <u>W</u>	101				
C. nucifera	101 <u>GHVTCRM</u> L-FT <u>MWIGNPITI</u> E <u>GSEFSNT</u> R <u>A</u> I--Y <u>IQNHAS</u> I <u>VDIFLIMW</u>	101				
Human LPAAT- β	151 <u>LPERCVQIAK</u> R <u>ELLFLGPV</u> --G <u>LIMYLOGV</u> F <u>ELINQRSS</u> T <u>AM</u> --V <u>MAIL</u>	160	170	180	190	200
Human LPAAT- α	151 <u>LPGRCVPIAK</u> R <u>ELLWAGSA</u> --G <u>LA</u> C <u>WLAGV</u> I <u>FIDRKRTG</u> D <u>AIS</u> --V <u>MSEV</u>	151				
Yeast LPAAT	151 F <u>PPGCCVTA</u> K <u>KSLKVPFL</u> --G <u>FM</u> ALSGT Y <u>FLDRSKRQE</u> A <u>ID</u> --T <u>INKG</u>	151				
E. coli LPAAT	151 <u>VOPPTVTVCK</u> K <u>SLLWIPFF</u> --G <u>OPLYWL</u> T <u>GN</u> I <u>LDNNR</u> T <u>K</u> A <u>HG</u> --T <u>IAEV</u>	151				
H. influenzae	151 <u>VOPRTVSVCK</u> K <u>SLLWIPFFF</u> T <u>GILYWWTGN</u> I <u>FLDREN</u> T <u>K</u> A <u>HN</u> --T <u>MSQL</u>	151				
S. typhimurium	151 <u>VOPPTVTVCK</u> K <u>SLLWIPFFF</u> T <u>GOLYWL</u> T <u>GN</u> I <u>LDNNRAK</u> A <u>HS</u> --T <u>IAAV</u>	151				
L. douglassii	151 A <u>PIGTVGVAK</u> KE <u>VIWYPLIG</u> Q--LY <u>TLAH</u> I <u>RDNSNPAA</u> A <u>IQSFTMKEA</u>	151				
C. nucifera	151 T <u>PGTVTIAK</u> KE <u>IIWYPLFG</u> Q <u>FTLYVLANH</u> Q <u>RDNSNPSA</u> A <u>IES</u> --I <u>KEV</u>	151				

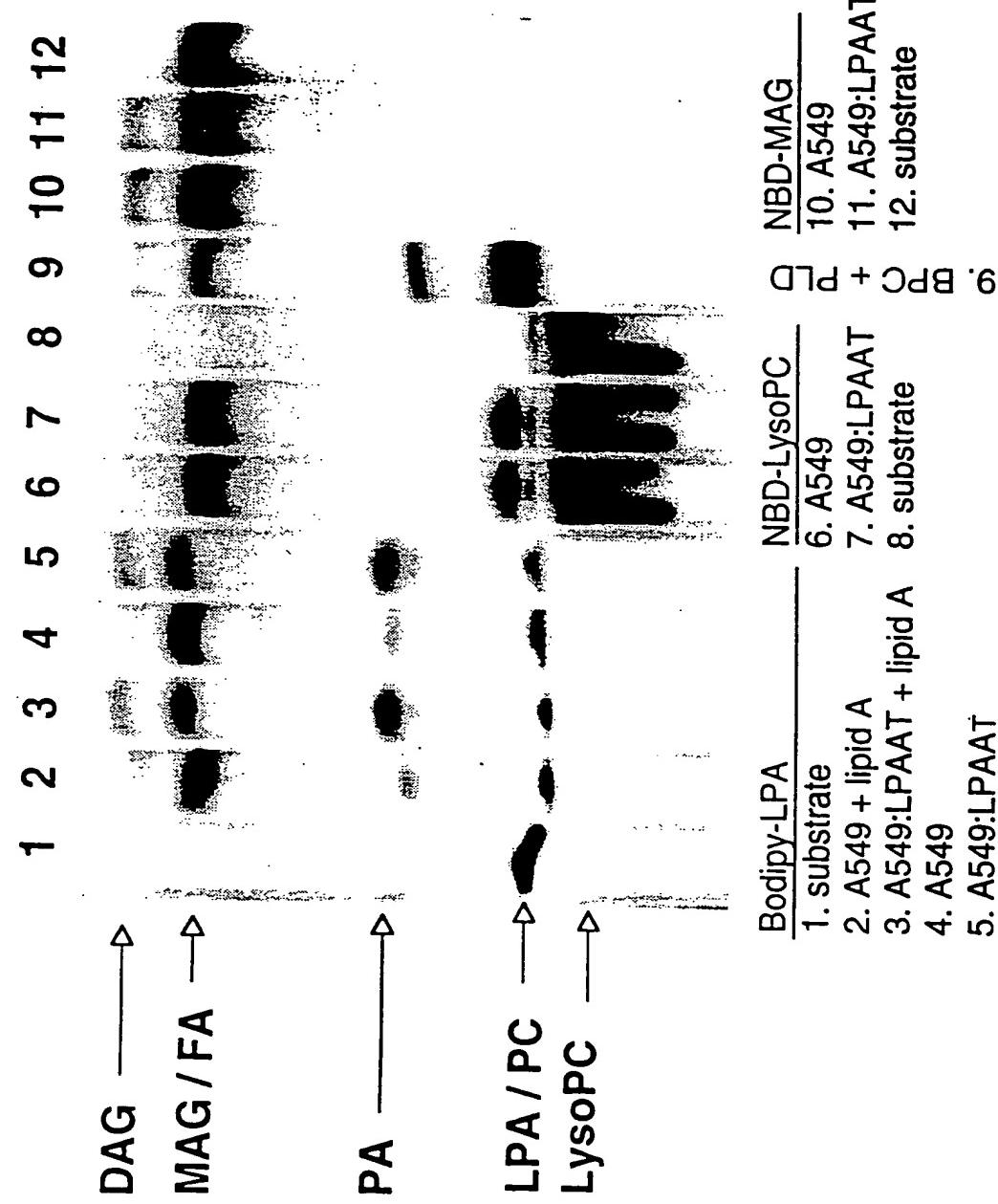
Figure 5 (continued)

Human LPAAT- β	201	<u>GERMIRENLK</u>	<u>VMTYPEGTRN</u>	<u>DNGDL</u> — <u>LPF</u>	<u>KKGAFYL</u> — <u>A</u>	<u>VOAQVPIVVP</u>
Human LPAAT- α	201	<u>AQILLLTQDVR</u>	<u>VWVFPEGTRN</u>	<u>HNGSY</u> — <u>LPF</u>	<u>KRGAFHL</u> — <u>A</u>	<u>VOAQVPIVPI</u>
Yeast LPAAT	201	<u>LENVKKNKRA</u>	<u>LWVFPEGTRS</u>	<u>YTSELTMILPF</u>	<u>KKGAFHL</u> — <u>A</u>	<u>QQCKIPIVPP</u>
E. coli LPAAT	201	<u>VNHFKRRRLS</u>	<u>IWMFPEGTRS</u>	<u>RGRGL</u> — <u>LPF</u>	<u>KTGAF</u> — <u>HAA</u>	<u>IAAGVPIIIPV</u>
H. influenzae	201	<u>ARRINEDNLS</u>	<u>IWMFPEGTRN</u>	<u>RGRGL</u> — <u>LPF</u>	<u>KTGAFTHAA</u>	<u>ISAGVPIIPV</u>
S. typhimurium	201	<u>VNHFKRRRLS</u>	<u>IWMFPEGTRS</u>	<u>RGRGL</u> — <u>LPF</u>	<u>KTGAFTHAA</u>	<u>IAAGVPIIPV</u>
L. douglassi	201	<u>VRVITTEKNL</u>	<u>LDMFPEGTRS</u>	<u>GDGRL</u> — <u>LPF</u>	<u>KKGFVHL</u> — <u>A</u>	<u>LQSHPIVPM</u>
C. nucifera	201	<u>ARAWKKNL</u>	<u>LITMFPEGTRS</u>	<u>KTGRL</u> — <u>LPF</u>	<u>KKGEFIHFTIA</u> <u>A</u>	<u>LQTRLPIVPM</u>
Human LPAAT- β	210					
Human LPAAT- α	210					
Yeast LPAAT	210					
E. coli LPAAT	210					
H. influenzae	210					
S. typhimurium	210					
L. douglassi	210					
C. nucifera	210					
Human LPAAT- β	220					
Human LPAAT- α	220					
Yeast LPAAT	220					
E. coli LPAAT	220					
H. influenzae	220					
S. typhimurium	220					
L. douglassi	220					
C. nucifera	220					
Human LPAAT- β	230					
Human LPAAT- α	230					
Yeast LPAAT	230					
E. coli LPAAT	230					
H. influenzae	230					
S. typhimurium	230					
L. douglassi	230					
C. nucifera	230					
Human LPAAT- β	240					
Human LPAAT- α	240					
Yeast LPAAT	240					
E. coli LPAAT	240					
H. influenzae	240					
S. typhimurium	240					
L. douglassi	240					
C. nucifera	240					
Human LPAAT- β	250					
Human LPAAT- α	250					
Yeast LPAAT	250					
E. coli LPAAT	250					
H. influenzae	250					
S. typhimurium	250					
L. douglassi	250					
C. nucifera	250					
Human LPAAT- β	260					
Human LPAAT- α	260					
Yeast LPAAT	260					
E. coli LPAAT	260					
H. influenzae	260					
S. typhimurium	260					
L. douglassi	260					
C. nucifera	260					
Human LPAAT- β	270					
Human LPAAT- α	270					
Yeast LPAAT	270					
E. coli LPAAT	270					
H. influenzae	270					
S. typhimurium	270					
L. douglassi	270					
C. nucifera	270					
Human LPAAT- β	280					
Human LPAAT- α	280					
Yeast LPAAT	280					
E. coli LPAAT	280					
H. influenzae	280					
S. typhimurium	280					
L. douglassi	280					
C. nucifera	280					
Human LPAAT- β	290					
Human LPAAT- α	290					
Yeast LPAAT	290					
E. coli LPAAT	290					
H. influenzae	290					
S. typhimurium	290					
L. douglassi	290					
C. nucifera	290					
Human LPAAT- β	300					
Human LPAAT- α	300					
Yeast LPAAT	300					
E. coli LPAAT	300					
H. influenzae	300					
S. typhimurium	300					
L. douglassi	300					
C. nucifera	300					

Figure 5 (continued)

Human LPAAT- β	310	<u>AMRTTFIHS</u>	KTPQENGATA	GSGVQPAQ*	330	340
Human LPAAT- α	301	<u>SMLTVFREIS</u>	T <u>DGRGGDYL</u>	K <u>PGGGG*</u>	350	
Yeast LPAAT	301	<u>QMVDILKEIG</u>	YSP <u>AINDTTL</u>	PFQATEYAA <u>L QHDKKWNKKT</u>		
E. coli LPAAT	301	-SIME <u>QKIAE</u>	<u>LDKEVA</u> - ER	<u>EAACKV*</u>		
H. influenzae	301	<u>TLM<u>E</u>KRIA<u>E</u></u>	<u>LDEETIA</u>	- K <u>GN*</u>		
S. typhimurium	301	<u>TALME<u>Q</u>KIA<u>E</u></u>	<u>LDKEVA</u> - ER	<u>EATCKV*</u>		
L. douglassi	301	<u>TYVRNIPASQ</u>	KPLGS--TNR	--S-K*		
C. nucifera	301	<u>TALYVTDHPE</u>	S <u>QKPLVSKGR</u>	<u>DASGRNS*</u>		
					360	370
					380	390
Human LPAAT- β	351					
Human LPAAT- α	351					
Yeast LPAAT	351	SNDVNTHNEG	SSVKRMH*			
E. coli LPAAT	351					
H. influenzae	351					
S. typhimurium	351					
L. douglassi	351					
C. nucifera	351					

Figure 6



TLC Analysis of Acyltransferase Activity

**Induction of TNF in A549 LPAAT or A549
cells stimulated with mTNF and IL-1 β**

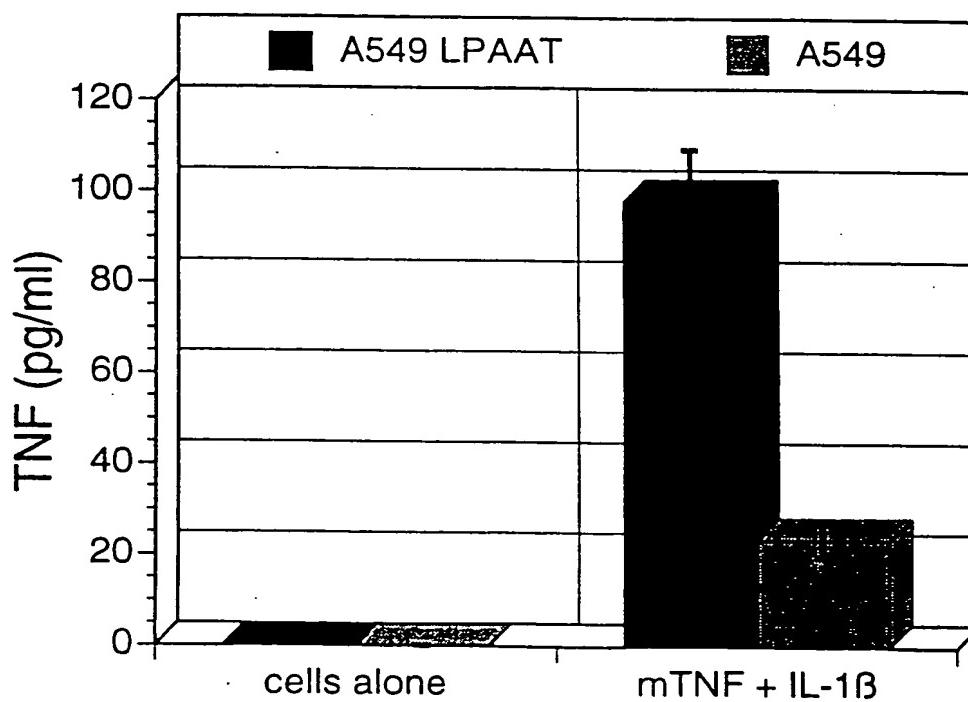


Figure 7

Title: METHOD OF SCREENING
COMPOUNDS THAT INHIBIT
LYSOPHOSPHATIDIC ACID
ACYLTRANSFERASE
Inventors: David W. LEUNG et al.
Docket No.: 077319-0382

**Induction of IL-6 in A549 LPAAT or A549
cells stimulated with mTNF and IL-1**

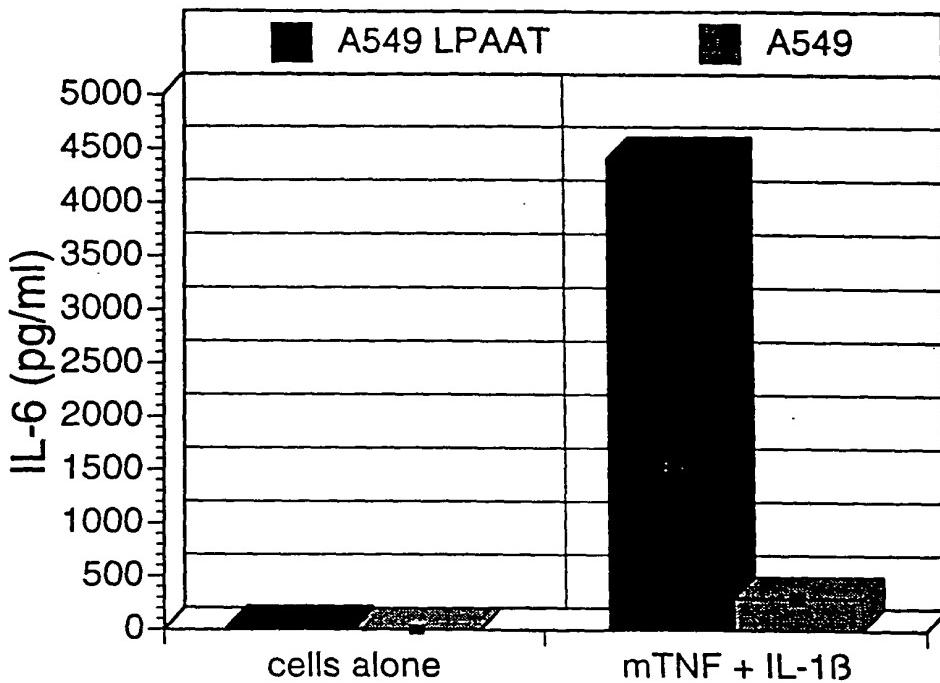


Figure 8

Title: METHOD OF SCREENING
 COMPOUNDS THAT INHIBIT
 LYSOPHOSPHATIDIC ACID
 ACYLTRANSFERASE
 Inventors: David W. LEUNG et al.
 Docket No.: 077319-0382

Figure 9 Translated sequence of human LPAAT- γ

TCTATGAAACCAACATACATGGCGTTGCATCACAGTTGGAGTCAGATGTGAGCCGGAG	60
GGCAGGGTGTCTGGCTTGCCACCCGGAAGCCCTGAGGGCAGCTGTTCCCCTGGCTCTGC	120
TGACCTTGTGCCTTGGACGGCTGTCCCTCAGCGAGGGCCGTGACACCGCTCCTGAGCAGC	180
GCC ATG GGC CTG CTG GCC TTC CTG AAG ACC CAG TTC GTG CTG CAC	225
Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His	
5 10	
CTG CTG GTC GGC TTT GTC TTC GTG GTG AGT GGT CTG GTC ATC AAC	270
Leu Leu Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn	
15 20 25	
TTC GTC CAG CTG TGC ACG CTG GCG CTC TGG CCG GTC AGC AAG CAG	315
Phe Val Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln	
30 35 40	
CTC TAC CGC CGC CTC AAC TGC CGC CTC GCA TAC TCA CTC TGG AGC	360
Leu Tyr Arg Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser	
45 50 55	
CAA CTG GTC ATG CTG CTG GAG TGG TGG TCC TGC ACG GAG TGT ACA	405
Gln Leu Val Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr	
60 65 70	
CTG TTC ACG GAC CAG GCC ACG GTA GAG CGC TTT GGG AAG GAG CAC	450
Leu Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His	
75 80 85	
GCA GTC ATC ATC CTC AAC CAC AAC TTC GAG ATC GAC TTC CTC TGT	495
Ala Val Ile Ile Leu Asn His Asn Phe Glu Ile Asp Phe Leu Cys	
90 95 100	
GGG TGG ACC ATG TGT GAG CGC TTC GGA GTG CTG GGG AGC TCC AAG	540
Gly Trp Thr Met Cys Glu Arg Phe Gly Val Leu Gly Ser Ser Lys	
105 110 115	
GTC CTC GCT AAG AAG GAG CTG CTC TAC GTG CCC CTC ATC GGC TGG	585
Val Leu Ala Lys Lys Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp	
120 125 130	
ACG TGG TAC TTT CTG GAG ATT GTG TTC TGC AAG CGG AAG TGG GAG	630
Thr Trp Tyr Phe Leu Glu Ile Val Phe Cys Lys Arg Lys Trp Glu	
135 140 145	
GAG GAC CGG' GAC ACC GTG GTC GAA GGG CTG AGG CGC CTG TCG GAC	675
Glu Asp Arg Asp Thr Val Val Glu Gly Leu Arg Arg Leu Ser Asp	
150 155 160	
TAC CCC GAG TAC ATG TGG TTT CTC CTG TAC TGC GAG GGG ACG CGC	720
Tyr Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu Gly Thr Arg	
165 170 175	
TTC ACG GAG ACC AAG CAC CGC GTT AGC ATG GAG GTG GCG GCT GCT	765
Phe Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala Ala Ala	
180 185 190	
AAG GGG CCTT CCT GTC CTC AAG TAC CAC CTG CTG CCG CGG ACC AAG	810
Lys Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr Lys	
195 200 205	
GGC TTC ACC ACC GCA GTC AAG TGC CTC CGG GGG ACA GTC GCA GCT	855
Gly Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala	
210 215 220	
GTC TAT GAT GTA ACC CTG AAC TTC AGA GGA AAC AAG AAC CCG TCC	900
Val Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser	
225 230 235	
CTG CTG GGG ATC CTC TAC GGG AAG AAG TAC GAG GCG GAC ATG TGC	945
Leu Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys	
240 245 250	
GTG AGG AGA TTT CCT CTG GAA GAC ATC CCG CTG GAT GAA AAG GAA	990
Val Arg Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu	
255 260 265	
GCA GCT CAG TGG CTT CAT AAA CTG TAC CAG GAG AAG GAC GCG CTC	1035

Title: METHOD OF SCREENING
COMPOUNDS THAT INHIBIT
LYSOPHOSPHATIDIC ACID
ACYLTRANSFERASE
Inventors: David W. LEUNG et al.
Docket No : 077319-0382

Figure 9 (continued)

Ala	Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu
270				275					280					
CAG	GAG	ATA	TAT	AAT	CAG	AAG	GGC	ATG	TTT	CCA	GGG	GAG	CAG	TTT
Gln	Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe
285					290				295					
AAG	CCT	GCC	CGG	AGG	CCG	TGG	ACC	CTC	CTG	AAC	TTC	CTG	TCC	TGG
Lys	Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp
300					305				310					
GCC	ACC	ATT	CTC	CTG	TCT	CCC	CTC	TTC	AGT	TTT	GTC	TTG	GGC	GTC
Ala	Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val
315					320				325					
TTT	GCC	AGC	GGA	TCA	CCT	CTC	CTG	ATC	CTG	ACT	TTC	TTG	GGG	TTT
Phe	Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe
330					335				340					
GTG	GGA	GCA	GCT	TCC	TTT	GGA	GTT	CGC	AGA	CTG	ATA	GGA	GTA	ACT
Val	Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	Leu	Ile	Gly	Val	Thr
345					350				355					
GAG	ATA	GAA	AAA	GGC	TCC	AGC	TAC	GGA	AAC	CAA	GAG	TTT	AAG	AAA
Glu	Ile	Glu	Lys	Gly	Ser	Ser	Tyr	Gly	Asn	Gln	Glu	Phe	Lys	Lys
360					365				370					
AAG	GAA	TAA	TTAATGGCTGTGACTGAAACACACGCGGCCCTGACGGTGGTATCCAGTT											1362
Lys	Glu	***												
AACT	AAA	ACC	AAC	ACA	CAC	AGAGT	GCAG	AAAAG	ACAATT	AGAAA	ACT	ATTTT	CTTATTAA	1422
CTGGT	GACT	AA	TTA	ACAAA	ACT	TGAG	CCAAG	AGAGT	AAAGA	ATT	CAGAAG	GCCT	TGTCAGG	1482
TGAAG	TCT	CAG	CCT	CCC	ACAG	CGC	CAGGG	TCC	CAGC	ATCT	CCAC	CGC	GCCC	TGGGAGG
TGGGT	CCGG	CCGG	GGAG	AGGG	CCT	CCCG	GGAC	GCC	GTCT	CTCC	CAGA	ACT	CCG	TTCCAAGAG
GGAC	ACT	TTGG	GT	CTT	CTC	CTTAA	ACT	AGAT	CAA	ATT	TTA	AAAAA	AAAAA	1660

Title: METHOD OF SCREENING
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 LYSOPHOSPHATIDIC ACID
 ACYLTRANSFERASE
 Inventors: David W. LEUNG et al.
 Docket No.: 077319-0382

Figure 10 Translated sequence of LPAAT- γ 2 cDNA

CACGCTGGCGCTCTGGCCGGTCAGCAAGCAGCTCACCGCCGCCCTCAACTGCCGCCCTGCC	61
TACTCACTCTGGAGCCTAGCACAAAACTAGAAGCAACCCAAAGCACCTGTCACTGGAGACT	121
AATTATGCAGGGACCCATACAGGGACCCTCTGCGGCCATCATGGAGAGCCTTCATCTGCC	181
CGTACAGTTTAAGCGAAAAGGAAGTATAACAACAAAGTCCATAACTGGTC <u>ATG</u> CTG	238
Met Leu	
CTG GAG TGG TGG TCC TGC ACG GAG TGT ACA CTG TTC ACG GAC CAG	283
Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu Phe Thr Asp Gln	
5 10 15	
GCC ACG GTA GAG CGC TTT GGG AAG GAG CAC GCA GTC ATC ATC CTC	328
Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala Val Ile Ile Leu	
20 25 30	
AAC CAC AAC TTC GAG ATC GAC TTC CTC TGT GGG TGG ACC ATG TGT	373
Asn His Asn Phe Glu Ile Asp Phe Leu Cys Gly Trp Thr Met Cys	
35 40 45	
GAG CGC TTC GGA GTG CTG GGG AGC TCC AAG GTC CTC GCT AAG AAG	418
Glu Arg Phe Gly Val Leu Gly Ser Ser Lys Val Leu Ala Lys Lys	
50 55 60	
GAG CTG CTC TAC GTG CCC CTC ATC GGC TGG ACG TGG TAC TTT CTG	463
Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp Thr Trp Tyr Phe Leu	
65 70 75	
GAG ATT GTG TTC TGC AAG CGG AAG TGG GAG GAG GAC CGG GAC ACC	508
Glu Ile Val Phe Cys Lys Arg Lys Trp Glu Asp Arg Asp Thr	
80 85 90	
GTG GTC GAA GGG CTG AGG CGC CTG TCG GAC TAC CCC GAG TAC ATG	553
Val Val Glu Gly Leu Arg Arg Leu Ser Asp Tyr Pro Glu Tyr Met	
95 100 105	
TGG TTT CTC CTG TAC TGC GAG GGG ACG CGC TTC ACG GAG ACC AAG	598
Trp Phe Leu Leu Tyr Cys Glu Gly Thr Arg Phe Thr Glu Thr Lys	
110 115 120	
CAC CGC GTT AGC ATG GAG GTG GCG GCT GCT AAG GGG CTT CCT GTC	643
His Arg Val Ser Met Glu Val Ala Ala Ala Lys Gly Leu Pro Val	
125 130 135	
CTC AAG TAC CAC CTG CTG CCG CGG ACC AAG GGC TTC ACC ACC GCA	688
Leu Lys Tyr His Leu Leu Pro Arg Thr Lys Gly Phe Thr Thr Ala	
140 145 150	
GTC AAG TGC CTC CGG GGG ACA GTC GCA GCT GTC TAT GAT GTA ACC	733
Val Lys Cys Leu Arg Gly Thr Val Ala Ala Val Tyr Asp Val Thr	
155 160 165	
CTG AAC TTC AGA GGA AAC AAG AAC CCG TCC CTG CTG GGG ATC CTC	778
Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu Leu Gly Ile Leu	
170 175 180	
TAC GGG AAG AAG TAC GAG GCG GAC ATG TGC GTG AGG AGA TTT CCT	823
Tyr Lys Lys Tyr Glu Ala Asp Met Cys Val Arg Arg Phe Pro	
185 190 195	
CTG GAA GAC ATC CCG CTG GAT GAA AAG GAA GCA GCT CAG TGG CTT	868
Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala Ala Gln Trp Leu	
200 205 210	
CAT AAA CTG TAC CAG GAG AAG GAC GCG CTC CAG GAG ATA TAT AAT	913
His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln Glu Ile Tyr Asn	
215 220 225	
CAG AAG GGC ATG TTT CCA GGG GAG CAG TTT AAG CCT GCC CGG AGG	958
Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys Pro Ala Arg Arg	
230 235 240	
CCG TGG ACC CTC CTG AAC TTC CTG TCC TGG GCC ACC ATT CTC CTG	1003
Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala Thr Ile Leu Leu	
245 250 255	
TCT CCC CTC TTC AGT TTT GTC TTG GGC GTC TTT GCC AGC GGA TCA	1048
Ser Pro Leu Phe Ser Phe Val Leu Gly Val Phe Ala Ser Gly Ser	

Title: METHOD OF SCREENING
COMPOUNDS THAT INHIBIT
LYSOPHOSPHATIDIC ACID
ACYLTRANSFERASE
Inventors: David W. LEUNG et al.
Docket No.: 077319-0382

Figure 10 (continued)

260	265	270	
CCT CTC CTG ATC CTG ACT TTC TTG GGG TTT GTG GGA GCA GCT TCC			1093
Pro Leu Leu Ile Leu Thr Phe Leu Gly Phe Val Gly Ala Ala Ser			
275	280	285	
TTT GGA GTT CGC AGA CTG ATA GGA GTA ACT GAG ATA GAA AAA GGC			1138
Phe Gly Val Arg Arg Leu Ile Gly Val Thr Glu Ile Glu Lys Gly			
290	295	300	
TCC AGC TAC GGA AAC CAA GAG TTT AAG AAA AAG GAA TAA TTAATGGC			1185
Ser Ser Tyr Gly Asn Gln Glu Phe Lys Lys Lys Glu ***			
305	310		
TGTGACTAACACACCGCGCCCTGACGGTGGTATCCAGTTAACTCAAAACCAACACAG			1245
AGTGCAGGAAAAGACAATTAGAAACTATTTCTTATTAACTGGTGACTAATATTAACAA			1305
AACTTGAGCCAAGAGTAAAGAATTCAAGAAGGCCCTGTCAGGTGAAGTCTTCAGCCTCCCAC			1365
AGCGCAGGGTCCCAGCATCTCACGCGCGCCCGTGGGAGGTGGGTCCGGCGAGAGGCC			1425
TCCCGCGGACGCCGTCTCTCCAGAACTCCGTTCCAAGAGGGACCTTGCGCTGCTTCTC			1485
TCCTTAAACTTAGATCAAATTAAAAA			1523

Title: METHOD OF SCREENING
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 Inventors: David W. LEUNG et al.
 Docket No.: 077319-0382

Figure 11 Translated sequence of human LPAAT- δ

TGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTCTAAGTCATGTGCCAAAGGCTGCCAG	61
GAAGGAGACGCCTCCTGAGTCCTGGATCTTCTTCTGGAAATCTTGACTGTGGG	121
<u>TAGTTATTATTTCTGAATAAGAGCGTCACGCATC</u> ATG GAC CTC GCG GGA CTG	175
Met Asp Leu Ala Gly Leu	
5	
CTG AAG TCT CAG TTC CTG TGC CAC CTG GTC TTC TGC TAC GTC TTT	220
Leu Lys Ser Gln Phe Leu Cys His Leu Val Phe Cys Tyr Val Phe	
10 15 20	
ATT GCC TCA GGG CTA ATC ATC AAC ACC ATT CAG CTC TTC ACT CTC	265
Ile Ala Ser Gly Leu Ile Ile Asn Thr Ile Gln Leu Phe Thr Leu	
25 30 35	
CTC CTC TGG CCC ATT AAC AAG CAG CTC TTC CGG AAG ATC AAC TGC	310
Leu Leu Trp Pro Ile Asn Lys Gln Leu Phe Arg Lys Ile Asn Cys	
40 45 50	
AGA CTG TCC TAT TGC ATC TCA AGC CAG CTG GTG ATG CTG CTG GAG	355
Arg Leu Ser Tyr Cys Ile Ser Ser Gln Leu Val Met Leu Leu Glu	
55 60 65	
TGG TGG TCG GGC ACG GAA TGC ACC ATC TTC ACG GAC CCG CGC GCC	400
Trp Trp Ser Gly Thr Glu Cys Thr Ile Phe Thr Asp Pro Arg Ala	
70 75 80	
TAC CTC AAG TAT GGG AAG GAA AAT GCC ATC GTG GTT CTC AAC CAC	445
Tyr Leu Lys Tyr Gly Lys Glu Asn Ala Ile Val Val Leu Asn His	
85 90 95	
AAG TTT GAA ATT GAC TTT CTG TGT GGC TGG AGC CTG TCC GAA CGC	490
Lys Phe Glu Ile Asp Phe Leu Cys Gly Trp Ser Leu Ser Glu Arg	
100 105 110	
TTT GGG CTG TTA GGG GGC TCC AAG GTC CTG GCC AAG AAA GAG CTG	535
Phe Gly Leu Leu Gly Ser Lys Val Leu Ala Lys Lys Glu Leu	
115 120 125	
GCC TAT GTC CCA ATT ATC GGC TGG ATG TGG TAC TTC ACC GAG ATG	580
Ala Tyr Val Pro Ile Ile Gly Trp Met Trp Tyr Phe Thr Glu Met	
130 135 140	
GTC TTC TGT TCG CGC AAG TGG GAG CAG GAT CGC AAG ACG GTT GCC	625
Val Phe Cys Ser Arg Lys Trp Glu Gln Asp Arg Lys Thr Val Ala	
145 150 155	
ACC AGT TTG CAG CAC CTC CGG GAC TAC CCC GAG AAG TAT TTT TTC	670
Thr Ser Leu Gln His Leu Arg Asp Tyr Pro Glu Lys Tyr Phe Phe	
160 165 170	
CTG ATT CAC TGT GAG GGC ACA CGG TTC ACG GAG AAG AAG CAT GAG	715
Leu Ile His Cys Glu Gly Thr Arg Phe Thr Glu Lys Lys His Glu	
175 180 185	
ATC AGC ATG CAG GTG GCC CGG GCC AAG GGG CTG CCT CGC CTC AAG	760
Ile Ser Met Gln Val Ala Arg Ala Lys Gly Leu Pro Arg Leu Lys	
190 195 200	
CAT CAC CTG TTG CCA CGA ACC AAG GGC TTC GCC ATC ACC GTG AGG	805
His His Leu Leu Pro Arg Thr Lys Gly Phe Ala Ile Thr Val Arg	
205 210 215	
AGC TTG AGA AAT GTA GTT TCA GCT GTA TAT GAC TGT ACA CTC AAT	850
Ser Leu Arg Asn Val Val Ser Ala Val Tyr Asp Cys Thr Leu Asn	
220 225 230	
TTC AGA AAT AAT GAA AAT CCA ACA CTG CTG GGA GTC CTA AAC GGA	895
Phe Arg Asn Asn Glu Asn Pro Thr Leu Leu Gly Val Leu Asn Gly	
235 240 245	
AAG AAA TAC CAT GCA GAT TTG TAT GTT AGG AGG ATC CCA CTG GAA	940
Lys Lys Tyr His Ala Asp Leu Tyr Val Arg Arg Ile Pro Leu Glu	
250 255 260	
GAC ATC CCT GAA GAC GAT GAC GAG TGC TCG GCC TGG CTG CAC AAG	985
Asp Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala Trp Leu His Lys	
265 270 275	

Title: METHOD OF SCREENING
 COMPOUNDS THAT INHIBIT
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 ACYLTRANSFERASE
 Inventors: David W. LEUNG et al.
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Figure 11 (continued)

CTC TAC CAG GAG AAG GAT GCC TTT CAG GAG GAG TAC TAC AGG ACG	1030
Leu Tyr Gln Glu Lys Asp Ala Phe Gln Glu Glu Tyr Tyr Arg Thr	
280 285 290	
GGC ACC TTC CCA GAG ACG CCC ATG GTG CCC CCC CGG CGG CCC TGG	1075
Gly Thr Phe Pro Glu Thr Pro Met Val Pro Pro Arg Arg Pro Trp	
295 300 305	
ACC CTC GTG AAC TGG CTG TTT TGG GCC TCG CTG GTG CTC TAC CCT	1120
Thr Leu Val Asn Trp Leu Phe Trp Ala Ser Leu Val Leu Tyr Pro	
310 315 320	
TTC TTC CAG TTC CTG GTC AGC ATG ATC AGG AGC GGG TCT TCC CTG	1165
Phe Phe Gln Phe Leu Val Ser Met Ile Arg Ser Gly Ser Ser Leu	
325 330 335	
ACG CTG GCC AGC TTC ATC CTC GTC TTC TTT GTG GCC TCC GTG GGA	1210
Thr Leu Ala Ser Phe Ile Leu Val Phe Phe Val Ala Ser Val Gly	
340 345 350	
GTT CGA TGG ATG ATT GGT GTG ACG GAA ATT GAC AAG GGC TCT GCC	1255
Val Arg Trp Met Ile Gly Val Thr Glu Ile Asp Lys Gly Ser Ala	
355 360 365	
TAC GGC AAC TCT GAC AGC AAG CAG AAA CTG AAT GAC TGA CTCAGGG	1301
Tyr Gly Asn Ser Asp Ser Lys Gln Lys Leu Asn Asp ***	
370 375	
AGGTGTCACCATCCGAAGGGAACCTTGGGGAACTGGTGGCCTCTGCATATCCTCCTTAGT	1361
GGGACACGGTGACAAGGCTGGGTGAGCCCTGCTGGGCACGGCGGAAGTCACGACCTCT	1421
CCAGCCAGGGAGTCTGGTCTCAAGGCCGGATGGGAGGAAGATGTTTGTAATCTTTTT	1481
TCCCCATGTGCTTAGTGGCTTTGGTTCTGTGATCATAGAAAGGGTATTTAGGCTGCAGGGGA	1541
GTGTGGTAGTGTGAACCTTGTTCTGTGATCATAGAAAGGGTATTTAGGCTGCAGGGGA	1601
GGGCAGGGCTGGGACCGAACAGGGACAAGTCCCCCTTCATCCTTGGTGTGAGTTTC	1661
TGTAACCTTGGTGTGCCAGAGATAAAGTGAAGATGACTAAATTAT	1721
GCCTCCAAGAAAAAAAAATTAAAGTGCTTTCTGGGTCAAAAAAAA	1774

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Figure 12

	10	20	30	40	50
LPAAT- γ_1	MGLLAFLKTQ	FVLHLLVGFV	FVVSGLVINF	VQ-LCTLALW	PVSKQLYRRL
LPAAT- γ_2	-----	-----	-----	-----	-----
LPAAT- δ	MDLAGLLKSQ	FLCHLVFCYV	FIASGLIINT	IQ-LFTLLLW	PINKQLFRKI
	60	70	80	90	100
LPAAT- γ_1	NCRLAYSLWS	QLVMLLEWWS	CTECTLFTDQ	ATVERFGKEH	AVIILNHNF
LPAAT- γ_2	-----	-----	-----	-----	-----
LPAAT- δ	NCRLSYCISS	QLVMLLEWWS	GTECTIFTDP	RAYLKYGKEN	AIIVVNLHKF
	110	120	130	140	150
LPAAT- γ_1	IDFLCGWTMC	ERFGVLGSSK	VLAKKELLYV	PLIGWTWYFL	EIVFCRKWE
LPAAT- γ_2	IDFLCGWTMC	ERFGVLGSSK	VLAKKELLYV	PLIGWTWYFL	EIVFCRKWE
LPAAT- δ	IDFLCGWSE	ERFGLLGGSK	VLAKKELAYV	PIIGWMWYFT	EMVFCRSRKWE
	160	170	180	190	200
LPAAT- γ_1	EDRDTVVEGL	RRLSDYPEYM	WFLLYCEGTR	FTETKHRVSM	EVAAAKGLPV
LPAAT- γ_2	EDRDTVVEGL	RRLSDYPEYM	WFLLYCEGTR	FTETKHRVSM	EVAAAKGLPV
LPAAT- δ	QDRKTVATSL	QHLRDYPEKY	FFLIHCEGTR	FTEKKHEISM	QVARAKGLPR
	210	220	230	240	250
LPAAT- γ_1	LKYHLLPRTK	GFTTAVKCLR	GTVAAVYDVT	LNF-RGNKNP	SLLGILYGKK
LPAAT- γ_2	LKYHLLPRTK	GFTTAVKCLR	GTVAAVYDVT	LNF-RGNKNP	SLLGILYGKK
LPAAT- δ	LKHLLPRTK	GFAITVRSLR	NVVSAYVDCT	LNF-RNNENP	TLLGVLngkk
	260	270	280	290	300
LPAAT- γ_1	YEADMCVRRF	PLEDIPLDEK	EAAQWLHKLY	QEKDALQEY	NQKGMPGEQ
LPAAT- γ_2	YEADMCVRRF	PLEDIPLDEK	EAAQWLHKLY	QEKDALQEY	NQKGMPGEQ
LPAAT- δ	YHADLYVRRI	PLEDIPEDDD	EC S AWLHKLY	QEKDAFQEY	YR T GTFP H TP
	310	320	330	340	350
LPAAT- γ_1	FKPARRPWTL	LNFLSWATIL	LSPLFSFVLG	VFASGSPLLI	---LTFLGFV
LPAAT- γ_2	FKPARRPWTL	LNFLSWATIL	LSPLFSFVLG	VFASGSPLLI	---LTFLGFV
LPAAT- δ	MVPPRRPWTL	VNWLF WAS ^L V	LYPFFQFLVS	MIRSGSSLTL	---ASFILVF
	360	370	380		
LPAAT- γ_1	GAASFGVRRL	IGVTEIEKGS	SYGNQEF--K	KKE*	
LPAAT- γ_2	GAASFGVRRL	IGVTEIEKGS	SYGNQEF--K	KKE*	
LPAAT- δ	FVASVGVRWM	IGVTEIDKGS	AYGNSDSKQK	LND*	

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Figure 13

